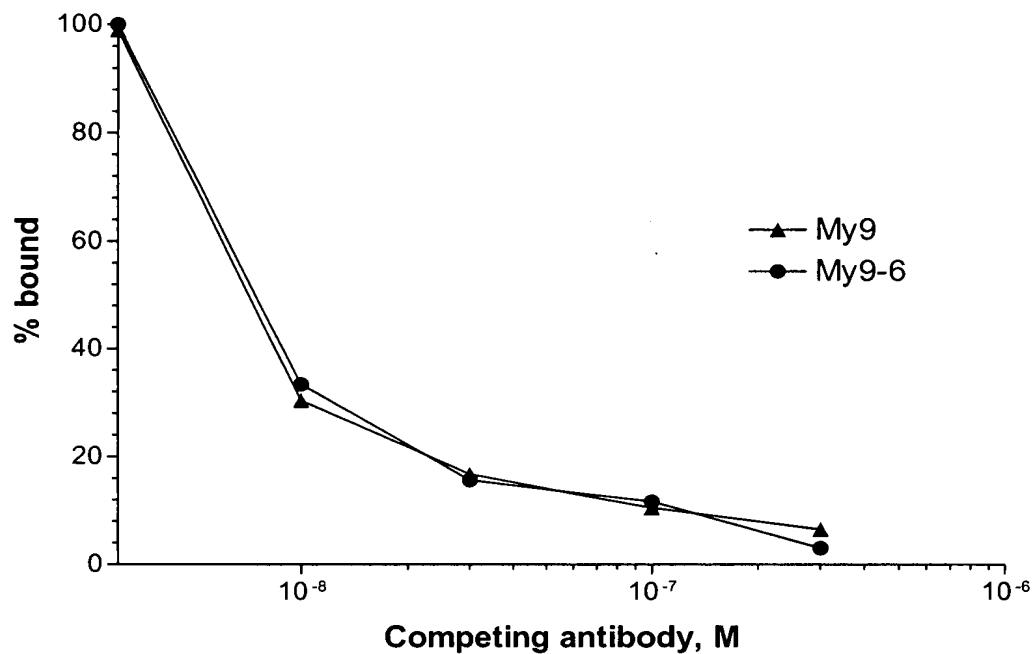


Attorney Docket No. A8427

**Figure 1**



Attorney Docket No. A8427

**Figure 2**

**My9-6 Light Chain Signal Sequence Degenerate Primers**

<u>Name</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>
Leaddeg1	TTTGATTCTGCTGTGGGTGTCCGGNACNTGYGG	17
Leaddeg2	TTTGATTCGCTGCTGCTGTGGGTNWSNGG	18
Leaddeg3	TTTGATTCCCAGGTGTTCATGCTGCTGYTNYTNTGGGT	19

Mixed bases: S = G+C, Y = C+T, W = A+T, N = A+T+G+C.

**Figure 3**

<b>127 Brookhaven Structure Files Used for Surface Predictions</b>									
2rcs	3hfl	3hfm	1aif	1a3r	1bbj	43c9	4fab	6fab	7fab
2gfb	2h1p	2hfl	1a6t	1axt	1bog	2hrp	2jel	2mcp	2pcp
1yuh	2bfv	2cgr	8fab	1ae6	1bvl	2dbl	2f19	2fb4	2fbj
1sm3	1tet	1vfa	glb2	1a4j	1cly	1vge	1yec	1yed	1yee
1nsn	1opg	1osp	1aj7	1ay1	1clz	1plg	1psk	1rmf	1sbs
1ncd	1nfd	1ngp	1acy	1afv	1cbv	1nld	1nma	1nmb	1nqb
1mcp	1mfb	1mim	15c8	1a5f	1axs	1mLb	1mpa	1nbv	1ncb
1jrh	1kb5	1kel	1ap2	1b2w	1adq	1kip	1kir	1lve	1mam
1igi	1igm	1igt	1ad0	1baf	1cfv	1igy	1ikf	1jel	1jhl
1gpo	1hil	1hyx	1a0q	1bjm	1clo	1iai	1ibg	1igc	1igf
1fpt	1frg	1fvc	1aqk	1bln	1d5b	1gaf	1ggi	1ghf	1gig
1fai	1fbi	1fdl	1ad9	1bbd	1f58	1fgv	1fig	1flr	1for
1dbl	1dfb	1a3l	1bfo	1eap	1dsf	1dvf			

Figure 4

Primer	Sequence	SEQ ID NO:
My96LCBsrG1	TACAGGTGTACACTCCGATATTGTGATCACCCAGACTCC	20
My96LCOL1	ACTGAAATCAAACGAACGTGGCTGCACCATCTG	21
My96LCOL2	GCCACAGTTGGTTGATTCCAGTTGGTGCCTG	22
My96HCBsrG1	TACAGGTGTACACTCCCAGTTAACGTGCAGAGTCTGG	23
My96HCOL1	CCACGGTCACCGTCTCCTAGCCTCACC	24
My96HCOL2	GAGGCTGAGGAACGGTAGCCGGTGGTCCC	25
My9-6LCNMLS	CAGGTGTACACTCCAATATTGCTACCCAGAGTCCATCATC	26
My9-6HCQP	CAGGTGTACACTCCCAGGTTAGCTGCAGCAGGCTGGGCTG	27
MY96HCQ64-1	AGAAGTCCAAAGGCAAGGCCAC	28
MY96HCQ64-2	CTTGCCTTGGAACTTCTGATTG	29
MY96HCQ105	CGATGGCCCTGGGGCTGAGGAGACGGTGACCGTGGTCCCTGGCCAGACATC	30
MY96LCEVGP	AGGTGTACACTCCGAGATGTGCTCACCCAGAGTCCAGGATCTGGCTGTGTCAGGAAAGGGTCACTATGAGC	31
MY96LCR45	GCCTGGTACCAACAGATACCAGGGCAGTCTCCAGACTTCTGATCTAC	32
MY96LCP80-1	AGCAGTGTCAACCTGAAGACCTGGC	33
MY96LCP80-2	GTCTCAGGTTAACACTGCTGATGG	34
MY96LCQ100	TTTTAAGCTTCGTTGATTCAGTTGGCTTGACCGAACGTCGG	35
My96icNM	CAGGTGTACACTCCAATATTGCTACCCAGAG	36
MY96LCK45	GCCTGGTACCAACAGATACCAGGGCAGTCTCTAAACTCTGATCTAC	37
My96HCApal	CGATGGCCCTGGGGCTGAGGAGACGGTGCACCG	38
huMy96LCOL1	ACTGAAATCAAACGTACGGTGGCTGCACCATCTG	39
huMy96LCOL2	GCCACCGTACGTTGATTCCAGTTGGTGCCTG	40
My96icEM	CAGGTGTACACTCCGAGATTATGCTCACCCAGAG	41
My96icNV	CAGGTGTACACTCCAATATTGTGCTCACCCAGAG	42
chMy96lcBsiW1	TTTCGTTACGTTGATTCAGTTGGTGC	43

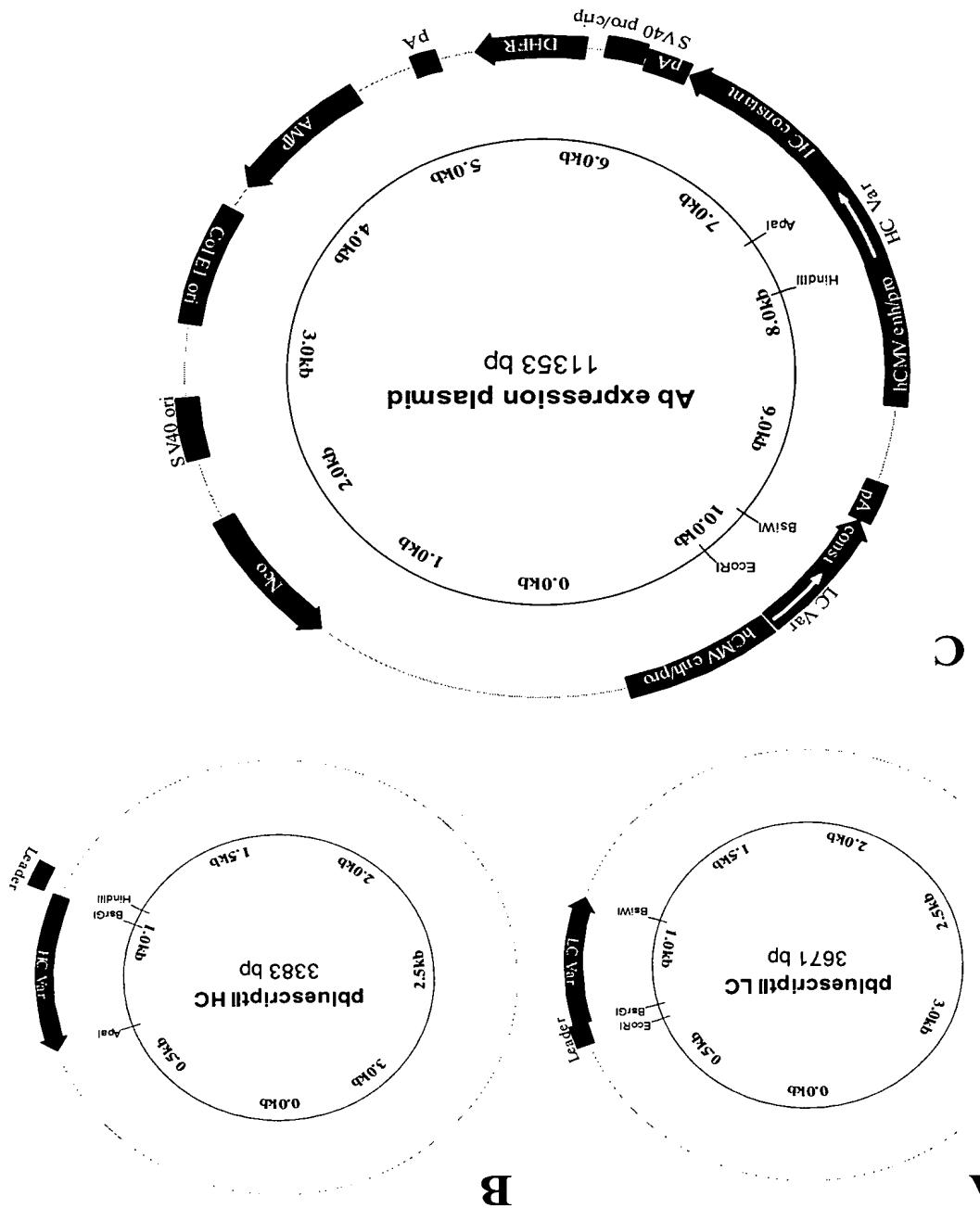


Figure 5

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**Figure 6A**

muMy9-6 Light Chain Amino Terminal Peptide Sequence												SEQ ID NO:
Edman Sequence	Kabat#	N	I	M	L	T	Q	S	P	S	S	23
Deg cDNA	D	I	V	I	T	T	Q	T	P	S	S	44
Sac1MK	E	L	D	I	V	X	T	Q	X	X		45
Primer	GG	GAG	CTC	GAY	ATT	GTG	MTS	ACM	CAR	WCT	MCA	
Signal Pep	N	I	M	L	T	Q	S	P	S	S	A	46
Deg cDNA												
												47

**Figure 6B**

MS-MS Sequence Analysis of muMy9-6 Light Chain CDR Peptide Fragments												SEQ ID NO:	
CDR1	<b>K</b>	<b>S</b>	<b>S</b>	<b>Q</b>	<b>S</b>	<b>V</b>	<b>F</b>	<b>F</b>	<b>S</b>	<b>S</b>	<b>Q</b>	<b>K</b>	48
1319Da	S	S	Q	S	V	F	F	S	S	Q	K		49
CDR2	K	L	L	I	Y	<b>W</b>	<b>A</b>	<b>S</b>	<b>T</b>	<b>R</b>	<b>E</b>	<b>S</b>	50
1122Da	K	L	L	I	Y	W	A	S	T	R	E		51

Figure 7

muMy9-6 Heavy Chain Internal/CDR3 Peptide Sequence														SEQ ID NO.	
1788 Da Sequence		(R)	Y	F	D	V	W	G	A	G	T	T	V	T	52
cDNA clone 2 (match)	E	V	R	<u>L</u>	R	Y	F	D	V	W	G	A	G	T	53
cDNA clone 1 (no match)	M	G	E	D	A	-	M	D	Y	W	G	Q	G	T	54

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**Figure 8A**

**Light Chain (sequential numbering) (SEQ ID NO:55):**

1 aacattatgctgacacagtcgcctatcatctctggctgtgtctgca  
1 N I M L T Q S P S S L A V S A

46 ggagaaaaggtaactatgagctgtaaagtccagtcaaagtgtttt  
16 G E K V T M S C K S S Q S V F  
CDR1

91 ttcaagttcaagtcaagaagaactacttggcctggtaaccaacagata  
31 F S S S Q K N Y L A W Y Q Q I  
CDR1

136 ccagggcagtctcctaaacttctgatctactggcatccactagg  
46 P G Q S P K L L I Y W A S T R  
CDR2

181 gaatctgggtccctgatcgcttacaggcagtggatctggaca  
61 E S G V P D R F T G S G S G T

226 gattttacttaccatcagcagtgtacaatctgaagacctggca  
76 D F T L T I S S V Q S E D L A

271 atttattactgtcatcaatacacctctcctcgccgacgttcggatgg  
91 I Y Y C H Q Y L S S R T F G G  
CDR3

316 ggcaccaaactggaaatcaaacga  
106 G T K L E I K R

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**Figure 8B**

**Heavy Chain (sequential numbering) (SEQ ID NO:56):**

1 caggtgcaactgcagcagcctgggctgaggtggtaagcctgg  
1 Q V Q L Q Q P G A E V V V K P G

46 gcctcagtgaagatgtcctgcaaggcttctggctacacatttacc  
16 A S V K M S C K A S G Y T F T

91 agttactatatacactggataaaggcagacacacctggacagggcctg  
31 S Y Y I H W I K Q T P G Q G L  
CDR1

136 gaatgggttggagttatccaggaaatgtatgtatcc  
46 E W V G V I Y P G N D D I S Y  
CDR2

181 aatcagaagttcaaaggcaaggccacattgactgcagacaaatcc  
61 N Q K F K G K A T L T A D K S  
CDR2

226 tccaccacagcctacatgcaactcagcagcctgacatctgaggac  
76 S T T A Y M Q L S S L T S E D

271 tctgcggctattactgtgcaagagaggttcgtctacggtaacttc  
91 S A V Y Y C A R E V R L R Y F  
CDR3

316 gatgtctgggcgcaggaccacggtcaccgtctcctca  
106 D V W G A G T T V T V S S

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**Figure 9**

**Murine My9-6 CDRs**

**Light Chain**

**SEQ ID NO:**

CDR1: K S S Q S V F F S S S Q K N Y L A

4

CDR2: W A S T R E S

5

CDR3: H Q Y L S S R T

6

**Heavy Chain**

CDR1: S Y Y I H

1

CDR2: V I Y P G N D D I S Y N Q K F K G

57

CDR3: E V R L R Y F D V

3

**AbM Heavy Chain**

CDR1: G Y T F T S Y Y I H

58

CDR2: V I Y P G N D D I S

59

CDR3: E V R L R Y F D V

3

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**Figure 10**

**GermLine Sequence Comparisons**

**Light Chain**

8-27*	NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSP	50
muMy9-6	...L.....FF..S.....I....	
8-27	KLLIYWASTRESGVPDFRTGSGSGTDFTLTISSVQAEDLAVYYCHQYLS	99
muMy9-6	.....S....I.....	

**Heavy Chain**

V102 <sup>#</sup>	-VQLQQPGAEVLVKPGASVKVSCKASGYTFTSYWMHWVKQRPGQGLEWIGR	50
muMy9-6	Q.....V.....M.....YI..I..T.....V.V	
V102	IHPSDSDTNYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA-	98
muMy9-6	.Y.GND.IS.....A....T.....R	

\* SEQ ID NO:60

Sequential residue numbering

# SEQ ID NO:61

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**Figure 11A**

**Light Chain Ten Most Homologous Sequences with Structures**

1										50
My96	NIMLTQSPSS	LA	VSA	GEKVT	MSCKSSQS	VF	FSSSQKNYLA	WYQQIPGQSP		
1sbs	DIVMSQSPSS	LA	VSVGEKVT	MTCKSSQS	L	YSSNQMN	YLA	WYQQKPGQSP		
1hil	DIVMTQSPSS	LT	VTAGEKVT	MSCTSSQS	LF	NSGKQKN	YLT	WYQQKPGQPP		
1a5f	DIVMTQSPSS	LT	VTGEKVT	MTCKSSQS	L	NSGAQKN	YLT	WYQQKPGQSP		
1a3r	DIVMTQSPSS	LT	VTGEKVT	MTCKSSQS	L	NSRTQKN	YLT	WYQQKPGQSP		
1frg	DIVMTQSPSS	LT	VTAGEKVT	MSCKSSQS	LF	NSGKRKN	F	WYHQKPGQPP		
1mcp	DIVMTQSPSS	LS	VSA	GERVT	MSCKSSQS	L	NSGNQKN	FLA	WYQQKPGQPP	
43c9	DVVMTQTPSS	LA	MSVGQKV	MSCKSSQS	L	NISNQKN	YLA	WYQQKPGQSP		
1lve	DIVMTQSPDS	LA	VSLGERAT	INCKSSQS	VL	YSSNSK	YLA	WYQQKPGQPP		
1ap2	DIVMTQSPSS	LT	VTAGEKVT	MSCKSSQS	L	NSGNQKN	YLT	WYQQKPGQPP		
1ncb	DIVMTQSPKF	MS	TSVGDRV	T	.....	AVV	WYQQKPGQSP			
										100
My96	KLLIYWASTR	ES	GVPDRFTG	SGSGTDFTL	T	ISSVQ	SEDLA	IYYCHQY	LSS	
1sbs	KLLIYWASTR	ES	GVPDRFTG	SGSGTDFTL	T	ISSV	EAEDLA	VYYCQQY	HSY	
1hil	KVLIYWASTR	ES	GVPDRFTG	SGSGTDFTL	T	ISSVQ	AEDLA	VYYCQND	YSN	
1a5f	KLLIYWASTR	ES	GVPDRFTG	SGSGTDFTL	S	ISGVQ	AEDLA	VYYCQNN	NY	
1a3r	KLLIYWASTR	ES	GVPDRFTG	SGSGTDFTL	S	ISGVQ	AEDLA	VYYCQNN	NY	
1frg	KLLIYWASTR	ES	GVPDRFSG	SGSGTDFTL	T	ITSVQ	AEDLA	IYYCQND	YSH	
1mcp	KLLIYGASTR	ES	GVPDRFTG	SGSGTDFTL	T	ISSVQ	AEDLA	VYYCQND	HSY	
43c9	KLLVYFASTR	ES	GVPDRFIG	SGSGTDFTL	T	ISSVQ	AEDQA	DYFCQQ	HYRA	
1lve	KLLIYWASTR	ES	GVPDRFSG	SGSGTDFTL	T	ISLQ	AEDVA	VYYCQ	YYST	
1ap2	KLLIYWASTR	ES	GVPDRFTG	SGSGTDFTL	T	ISSVQ	AEDLA	VYYCQND	SY	
1ncb	KLLIYWASTR	HIGVPDRFAG	SGSGTDFTL	T	ISSVQ	AEDLA	LYYCQQ	HYSP		
										115
My96	.RTFGGGT	KL	EIKRA	(SEQ	ID	NO:62)				
1sbs	PFTFGSGT	KL	EIKRA	(SEQ	ID	NO:63)				
1hil	PLTFGGGT	KL	ELKRA	(SEQ	ID	NO:64)				
1a5f	PLTFGAGT	KL	ELKRA	(SEQ	ID	NO:65)				
1a3r	PLTFGAGT	KL	ELKRA	(SEQ	ID	NO:66)				
1frg	PLTFGAGT	KL	ELKRA	(SEQ	ID	NO:67)				
1mcp	PLTFGAGT	KL	EIKRA	(SEQ	ID	NO:68)				
43c9	PRTFGGGT	KL	EIK	(SEQ	ID	NO:69)				
1lve	PYSFGQGT	KL	EIKR	(SEQ	ID	NO:70)				
1ap2	PLTFGAGT	KL	EPG	(SEQ	ID	NO:71)				
1ncb	PWTFGGGT	KL	EIKRA	(SEQ	ID	NO:72)				

Residue numbering is sequential

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**Figure 11B**

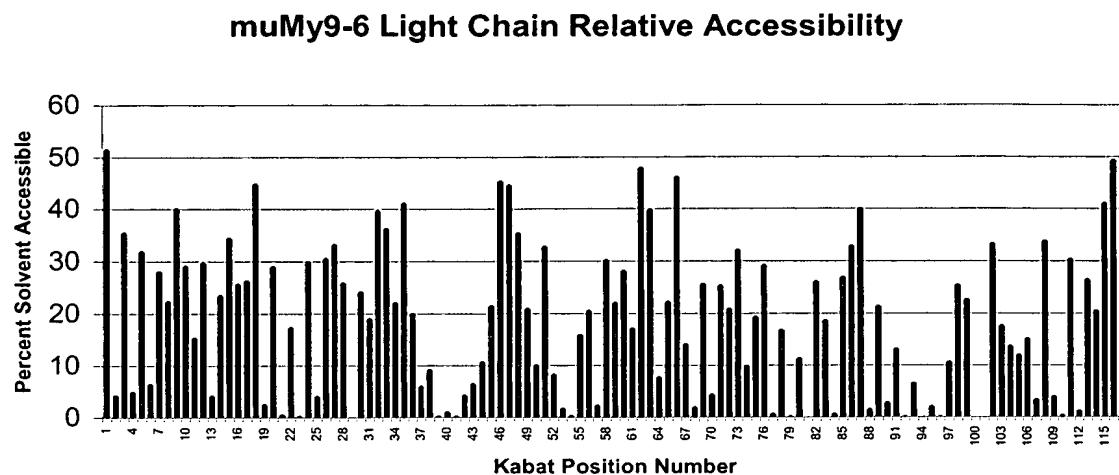
**Heavy Chain Ten Most Homologous Sequences with Structures**

1	50
My96	QVQLQQPGAE VVKPGASVKM SCKASGYTFT SYYIHWIKQT PGQGLEWVG
1plg	QIQLQQSGPE LVRPCASVKI SCKASGYTFT DYYIHWVKQR PGEGLEWIGW
1ae6	QIQLQQSGPE LVRPCASVKI SCKASGYTFT DYYINWMKQK PGQGLEWIGW
1for	QGQLQQSGAE LVRPCSSVVI SCKASGYAFS SFWVNWVKQR PGQGLEWIGQ
1igy	.VKLQESGAE LARPGASVKM SCKASGYTFT TYTIHWIKQR PGQGLEWIGY
1bbj	XVQLQQSDAE LVRPCASVKI SCKASGYTFT DHAIHWAKQK PEQGLEWIGY
1nqb	.VQLQQSGAE LVRPCASVKL SCKASGYTFT SYWMHWVKQR PGRGLEWIGR
1mim	.QLQQSGTV LARPGASVKM SCKASGYSFT RYWMHWIKQR PGQGLEWIGA
1a6t	EVQLQQSGPD LVRPCASVKI SCKASGYSFS TYYMHWVKQS HGKSLEWIGR
1d5b	QVQLQQSGAE LMKPGASVKI SCKATGYTFS SFWIEWVKQR PGHGLEWIGE
1fai	QVQLQQSGAE LVRAGSSVKM SCKASGYTFT SYGVVNWVKQR PGQGLEWIGY
	100
My96	IYPGNDDISY NQKFKGKATL TADKSSTAY MQLSSLTSED SAVYYCAREV
1plg	IYPGSGNTKY NEKFKGKATL TVDTSSSTAY MQLSSLTSED SAVYFCARGG
1ae6	IDPGSGNTKY NEKFKGKATL TVDTSSSTAY MQLSSLTSED TAVYFCAREK
1for	IYPGDGDNKY NGKFKGKATL TADKSSTAY MQLYSLTSED SAVYFCARSG
1igy	INPSSVYTNY NQRFKDKATL TRDRSSNTAN IHLSLLTSD SAVYYCVREG
1bbj	ISPGNDDIKY NEKFKGKATL TADKSSSTAY MQLNSLTSED SAVYFCKRSY
1nqb	IDPNSSGTTKY NEKFKSKATL TVDKPSSTAY MQLSSLTSED SAVYYCARYD
1mim	IYPGNSDTSY NQKFEKGAKL TAVTSASTAY MELSSLTHED SAVYYCSRDY
1a6t	VDPDNGGTSF NQKFKGKAIL TVDKSSSTAY MELGSLTSED SAVYYCARRD
1d5b	ILPGSGGTHY NEKFKGKATF TADKSSNTAY MQLSSLTSED SAVYYCARGH
1fai	INPGKGYLSY NEKFKGKTTL TVDRSSSTAY MQLRSLTSED AAVYFCARSF
	124
My96	RLRY..... FDVGAGTTV TVSS (SEQ ID NO:73)
1plg	K.....FA MDYWGQGTSV TVSS (SEQ ID NO:74)
1ae6	TTYY.....YA MDYWGQGTSV TVSS (SEQ ID NO:75)
1for	NYPY.....A MDYWGQGTSV TVSS (SEQ ID NO:76)
1igy	.....E VPYWGQGTTV TVSS (SEQ ID NO:77)
1bbj	YGHW..... GQGTTL TVSS (SEQ ID NO:78)
1nqb	YYGS.....SY FDYWGQGTTV TVSS (SEQ ID NO:79)
1mim	GYYF..... DFWGQGTTL TVSS (SEQ ID NO:80)
1a6t	DY.....Y FDFWGQGTSV TVSS (SEQ ID NO:81)
1d5b	SYYFY.....D GDYWGQGTSV TVSS (SEQ ID NO:82)
1fai	YGGSDLAVYY FDSWGQGTTL TVSS (SEQ ID NO:83)

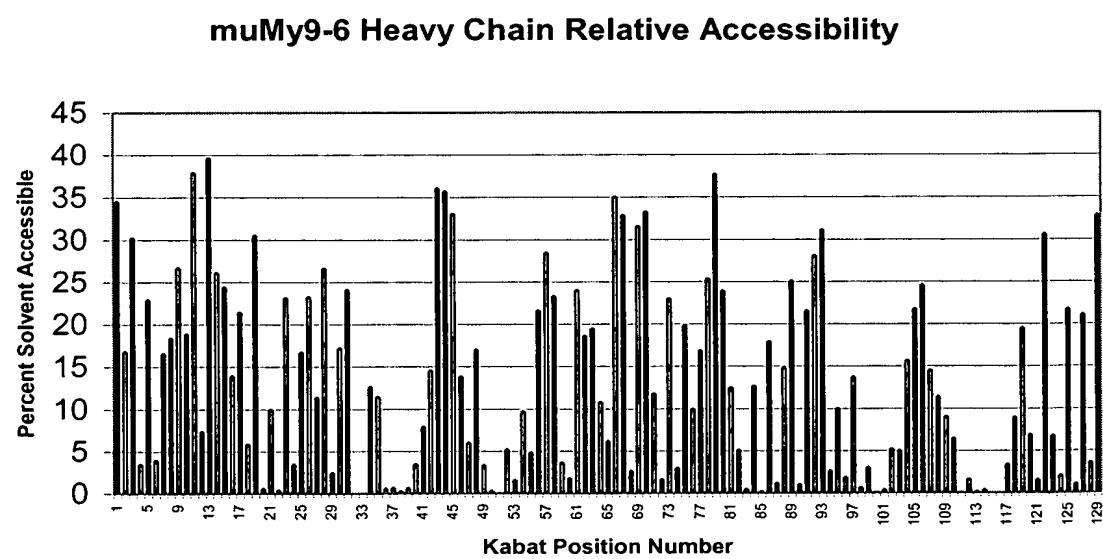
Residue numbering is sequential

Attorney Docket No. A8427

**Figure 12A**



**Figure 12B**



Attorney Docket No. A8427

Figure 13A

muMy9-6 Light Chain Surface Residues						
Kabat Position #	Average accessibility	> 30% Ave acc	25%-35% Ave acc	Identical flank		muMy9-6 surface
1	51.46	1				N1
3	35.42	3				M3
5	31.82	5	5	NA		T5
7	28.04		7	26.17		
9	40.08	9				S9
10	29.04		10	27.76		
12	29.63		12	22.32	other A's	
15	34.39	15	15	18.20	33.36	A15
16	25.61		16	NA		
17	26.21		17	25.11		
18	44.83	18				K18
20	28.91		20	29.11		
40	45.25	40				P40
41	44.52	41				G41
42	35.34	42				Q42
45	32.68	45	45	32.58		K45
57	39.81	57				G57
60	46.07	60				D60
63	25.60		63	26.87		
65	25.28		65	24.07		
67	32.05	67	67		1live left out	S67
70	29.16		70	29.28	30.13	D70
76	26.02		76	24.29		
79	26.83		79	NA		
80	32.78	80	80	NA		S80
81	39.95	81				E81
100	33.79	100	100	34.05		G100
103	30.30	103	103	30.30		K103
105	26.42		105	26.96		
107	41.06	107				K107
108	49.29	108				R108
109	41.85	109				A109

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**Figure 13B**

<b>muMy9-6 Heavy Chain Surface Residues</b>					
Kabat Position #	Average accessibility	> 30% Ave accessibility	25%-35% Ave acc	Identical flank	muMy9-6 surface
1	40.08	1			Q1
3	38.62	3			Q3
5	28.06		5	NA	
9	35.98	9			A9
11	48.07	11			V11
13	49.75	13			K13
14	32.39	14	14	32.20	P14
15	30.69	15	15	31.84	G15
17	26.01		17	26.67	
19	37.64	19			K19
23	29.92		23	30.11	K23
26	29.48		26	31.43	G26
28	33.67	28	28	35.59	T28
41	44.46	41			P41
42	46.28	42			G42
43	42.00	43			Q43
52B	25.21		52B	25.21	
53	28.84		53	28.84	
56	29.08		56	29.08	
61	43.12	61			Q61
62	44.46	62			K62
64	38.56	64			K64
65	41.85	65			G65
68	28.38		68	28.30	
70	25.14		70	28.21	
73	32.97	73	73	35.71	K73
74	47.68	74			S74
75	26.67		75	27.22	
82B	32.62	82B	82B	30.58	S82B
83	26.03		83	26.52	
84	35.34	84			S84
85	37.78	85			E85
105	36.29	105			A105
108	25.74		108	28.73	
110	26.94		110	23.38	
112	41.61	112			S112

Figure 14

**muMy9-6 Surface Residues  
within 5 Å of a CDR Residue**

Light chain	Heavy chain
N1	Q1
M3	T28
T5	K64
K45	K73
G57	
D60	
S67	
D70	

Figure 15

Antibody	Top Five Most Homologous Human Antibody Surfaces		SEQ ID NO:
	Light Chain	Heavy Chain	
muMy9-6	N M T S A K P G Q K G D S D S E G K K R A	84	Q Q A V K P G K G T P G Q Q K K G K S S E A S
21H9	D Q T S V R P G E K G S S D P E G K K R T	85	Q Q A V K P G K G T P G Q Q K Q G T P S S E K S
EL-14	D V T S V R P G K K G S S D P E G K K R -	86	Q Q A A K P G K G T P G Q Q K Q G G S S E Q S
CLL-412	D Q T S V R P G K K G S S D P E Q K K R T	87	Q Q A V K P G K G T P G Q Q K Q G T S S S E Q S
LC3bPB	E V T G P R P G Q R G D S D P E Q K K R -	88	- Q A V K P G K G T P G Q Q K Q G K S S S E Q S
CLL1.69	D V T L L P P G Q R G D A D A E Q K K R -	89	Q Q A V K P G K G T P G Q Q K Q G K S S S E Q S

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**Figure 16A**

**Humanized My9-6 Light Chain Versions**

Kabat #	10	20	27b	34	44
muMy9-6	<u>NIMLTQSPSS</u>	LAVSAGEKVT	MSCKSSQSVF	FSSSQKNYLA	WYQQIPGQSP
huMy9-6 V1.0	<u>EIVLTQSPGS</u>	LAVSPGERVT	MSCKSSQSVF	FSSSQKNYLA	WYQQIPGQSP
huMy9-6 V1.1	N.M.	.....	.....	.....	.....
huMy9-6 V1.2	N.M.	.....	.....	.....	.....
huMy9-6 V1.3	E.V.	.....	.....	.....	.....
huMy9-6 V1.4	N.M.	.....	.....	.....	.....
huMy9-6 V1.5	N.M.	.....	.....	.....	.....
huMy9-6 V1.6	E.V.	.....	.....	.....	.....
huMy9-6 V1.7	E.V.	.....	.....	.....	.....
huMy9-6 V1.8	E.M.	.....	.....	.....	.....
huMy9-6 V1.9	E.M.	.....	.....	.....	.....
huMy9-6 V1.10	E.M.	.....	.....	.....	.....
huMy9-6 V1.11	E.M.	.....	.....	.....	.....
huMy9-6 V1.12	N.V.	.....	.....	.....	.....
huMy9-6 V1.13	N.V.	.....	.....	.....	.....
huMy9-6 V1.14	N.V.	.....	.....	.....	.....
huMy9-6 V1.15	N.V.	.....	.....	.....	.....
Kabat #	54	64	74	84	94
muMy9-6	<u>KLLIYWASTR</u>	ESGVPDFRTG	SGSGTDFTLT	ISSVQSEDLA	IYYCHQYLSS
huMy9-6 V1.0	<u>RLLIYWASTR</u>	ESGVPDFRTG	SGSGTDFTLT	ISSVQPEDLA	IYYCHQYLSS
huMy9-6 V1.1	K.	.....	.....	.....	.....
huMy9-6 V1.2	K.	.....	.....	.....	.....
huMy9-6 V1.3	R.	.....	.....	.....	.....
huMy9-6 V1.4	R.	.....	.....	.....	.....
huMy9-6 V1.5	R.	.....	.....	.....	.....
huMy9-6 V1.6	K.	.....	.....	.....	.....
huMy9-6 V1.7	K.	.....	.....	.....	.....
huMy9-6 V1.8	R.	.....	.....	.....	.....
huMy9-6 V1.9	R.	.....	.....	.....	.....
huMy9-6 V1.10	K.	.....	.....	.....	.....
huMy9-6 V1.11	K.	.....	.....	.....	.....
huMy9-6 V1.12	R.	.....	.....	.....	.....
huMy9-6 V1.13	R.	.....	.....	.....	.....
huMy9-6 V1.14	K.	.....	.....	.....	.....
huMy9-6 V1.15	K.	.....	.....	.....	.....
Kabat #	108				
muMy9-6	RTFGGGTKLE	IKR	(SEQ ID NO:8)		
huMy9-6 V1.0	RTFG <u>Q</u> GTKLE	IKR	(SEQ ID NO:10)		
huMy9-6 V1.1	.....	....			
huMy9-6 V1.2	.....	....			
huMy9-6 V1.3	.....	....			
huMy9-6 V1.4	.....	....			
huMy9-6 V1.5	.....	....			
huMy9-6 V1.6	.....	....			
huMy9-6 V1.7	.....	....			
huMy9-6 V1.8	.....	....			
huMy9-6 V1.9	.....	....			
huMy9-6 V1.10	.....	....			
huMy9-6 V1.11	.....	....			
huMy9-6 V1.12	.....	....			
huMy9-6 V1.13	.....	....			
huMy9-6 V1.14	.....	....			
huMy9-6 V1.15	.....	....			

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**Figure 16B**

**Humanized My9-6 Heavy Chain Versions**

Kabat #	10	20	30	40	50
muMy9-6	QVQLQQPGAE	VVKPGASVVM	SCKASGYTFT	SYYIHWIKQT	PGQGLEWVGV
huMy9-6 V1.0	QVQLQQPGAE	VVKPGASVVM	SCKASGYTFT	SYYIHWIKQT	PGQGLEWVGV
huMy9-6 V1.1	.....	.....	.....	.....	.....
huMy9-6 V1.2	.....	.....	.....	.....	.....
huMy9-6 V1.3	.....	.....	.....	.....	.....
huMy9-6 V1.4	.....	.....	.....	.....	.....
huMy9-6 V1.5	.....	.....	.....	.....	.....
huMy9-6 V1.6	.....	.....	.....	.....	.....
huMy9-6 V1.7	.....	.....	.....	.....	.....
huMy9-6 V1.8	.....	.....	.....	.....	.....
huMy9-6 V1.9	.....	.....	.....	.....	.....
huMy9-6 V1.10	.....	.....	.....	.....	.....
huMy9-6 V1.11	.....	.....	.....	.....	.....
huMy9-6 V1.12	.....	.....	.....	.....	.....
huMy9-6 V1.13	.....	.....	.....	.....	.....
huMy9-6 V1.14	.....	.....	.....	.....	.....
huMy9-6 V1.15	.....	.....	.....	.....	.....
Kabat #	59	69	79	86	96
muMy9-6	IYPGNDDISY	NQKFKGKATL	TADKSSTTAY	MQLSSLTSED	SAVYYCAREV
huMy9-6 V1.0	IYPGNDDISY	NQKF <u>Q</u> GKATL	TADKSSTTAY	MQLSSLTSED	SAVYYCAREV
huMy9-6 V1.1	.....	K.....	.....	.....	.....
huMy9-6 V1.2	.....	Q.....	.....	.....	.....
huMy9-6 V1.3	.....	K.....	.....	.....	.....
huMy9-6 V1.4	.....	Q.....	.....	.....	.....
huMy9-6 V1.5	.....	K.....	.....	.....	.....
huMy9-6 V1.6	.....	Q.....	.....	.....	.....
huMy9-6 V1.7	.....	K.....	.....	.....	.....
huMy9-6 V1.8	.....	Q.....	.....	.....	.....
huMy9-6 V1.9	.....	K.....	.....	.....	.....
huMy9-6 V1.10	.....	Q.....	.....	.....	.....
huMy9-6 V1.11	.....	K.....	.....	.....	.....
huMy9-6 V1.12	.....	Q.....	.....	.....	.....
huMy9-6 V1.13	.....	K.....	.....	.....	.....
huMy9-6 V1.14	.....	Q.....	.....	.....	.....
huMy9-6 V1.15	.....	K.....	.....	.....	.....
Kabat #	105	112			
muMy9-6	RLRYFDVWGA	GTTVTVSS		(SEQ ID NO: 7)	
huMy9-6 V1.0	RLRYFDVW <u>G</u> Q	GTTVTVSS		(SEQ ID NO: 9)	
huMy9-6 V1.1	.....	.....			
huMy9-6 V1.2	.....	.....			
huMy9-6 V1.3	.....	.....			
huMy9-6 V1.4	.....	.....			
huMy9-6 V1.5	.....	.....			
huMy9-6 V1.6	.....	.....			
huMy9-6 V1.7	.....	.....			
huMy9-6 V1.8	.....	.....			
huMy9-6 V1.9	.....	.....			
huMy9-6 V1.10	.....	.....			
huMy9-6 V1.11	.....	.....			
huMy9-6 V1.12	.....	.....			
huMy9-6 V1.13	.....	.....			
huMy9-6 V1.14	.....	.....			
huMy9-6 V1.15	.....	.....			

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**Figure 17**

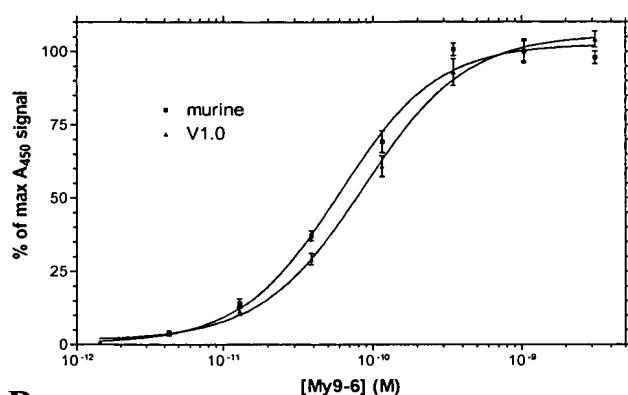
<b>My9-6 K<sub>D</sub> Values</b>			
	Direct on Membranes	Competitive on Membranes	Direct on Cells
	pM	pM	nM
murine	51.34+/-8.74	173.64+/-39.29	1.10+/-0.13
V1.0	66.53+/-17.83	209.00+/-52.37	1.02+/-0.04
V1.1	83.57+/-13.82	279.50+/-152.03*	1.07+/-0.11*
V1.3	63.95+/-0.64*	203.05+/-153.83*	1.16+/-0.39*
V1.6	56.10+/-15.13*	216.50+/-70.00*	0.97+/-0.08*

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**Figure 18**

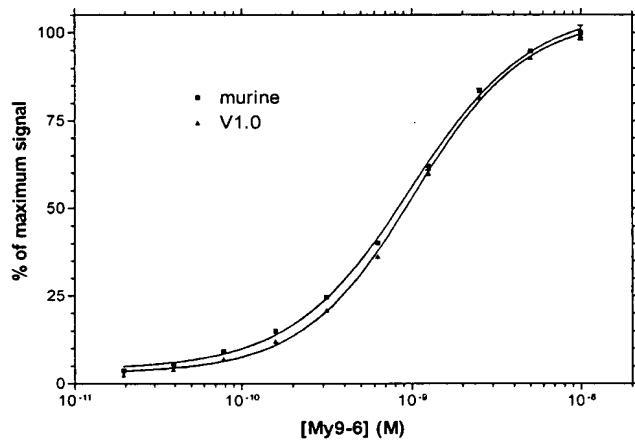
**A**

Direct Binding of Humanized My9-6 V1.0 to HL-60 Membranes



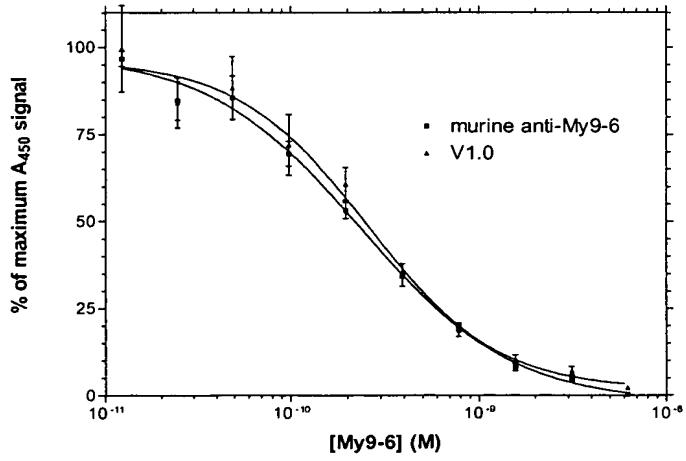
**B**

Direct Binding of Humanized My9-6 on HL-60 Cells



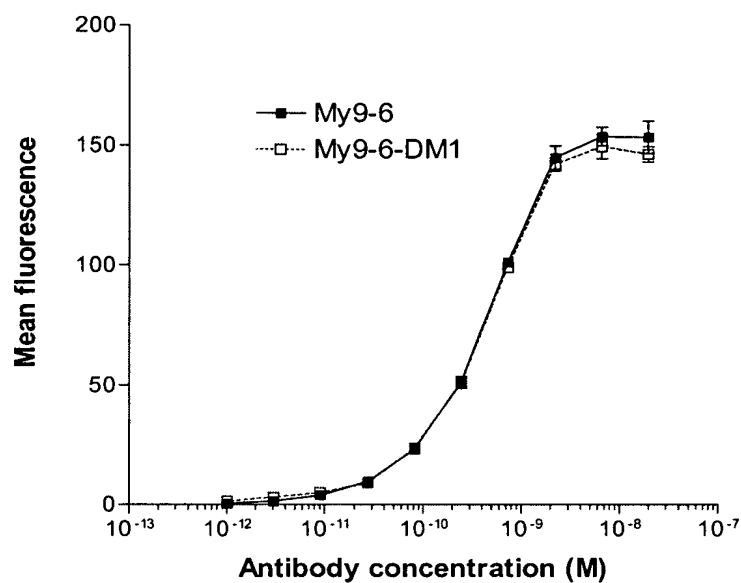
**C**

Competitive Binding of Humanized My9-6 V1.0 on HL-60 Membranes

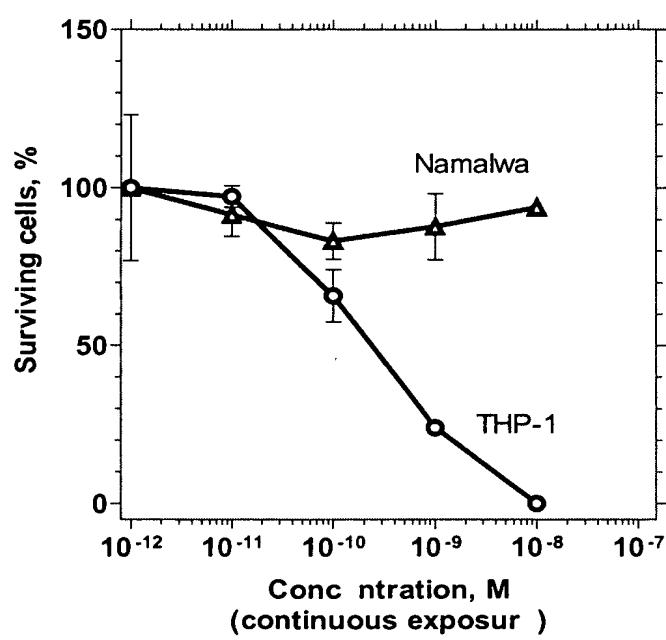


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**Figure 19**

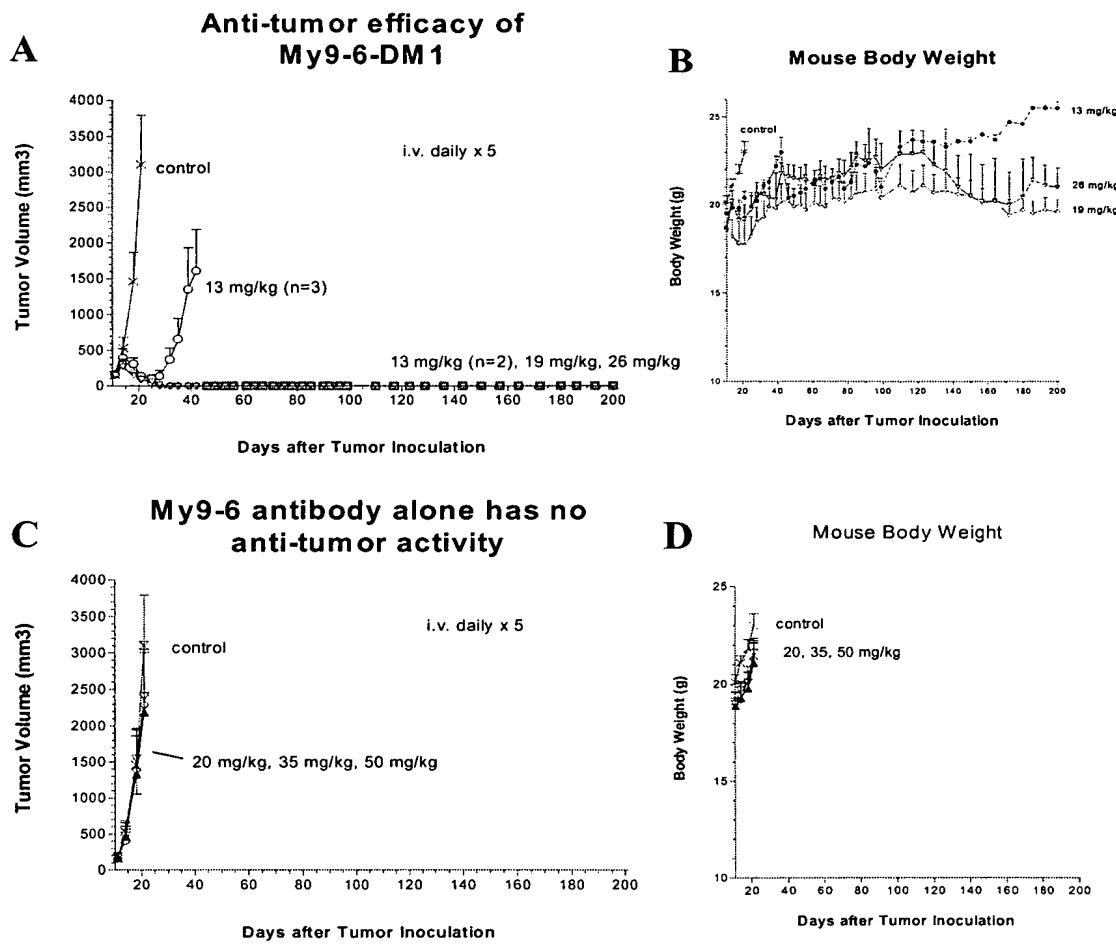


**Figure 20**



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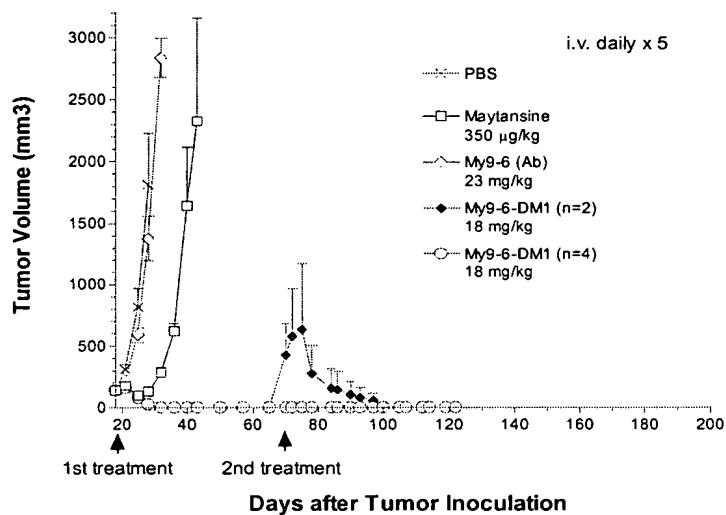
**Figure 21**



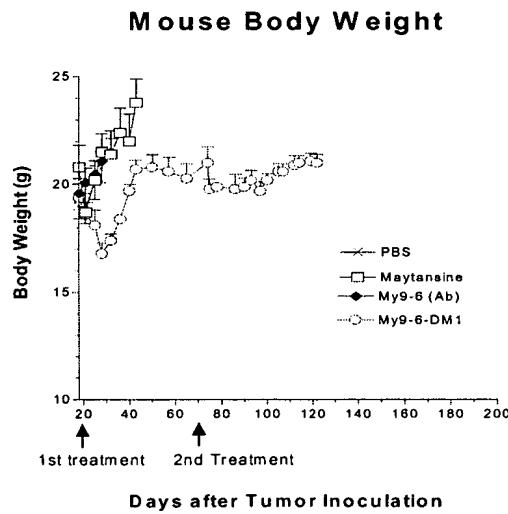
Attorney Docket No. A8427

**Figure 22**

**A**

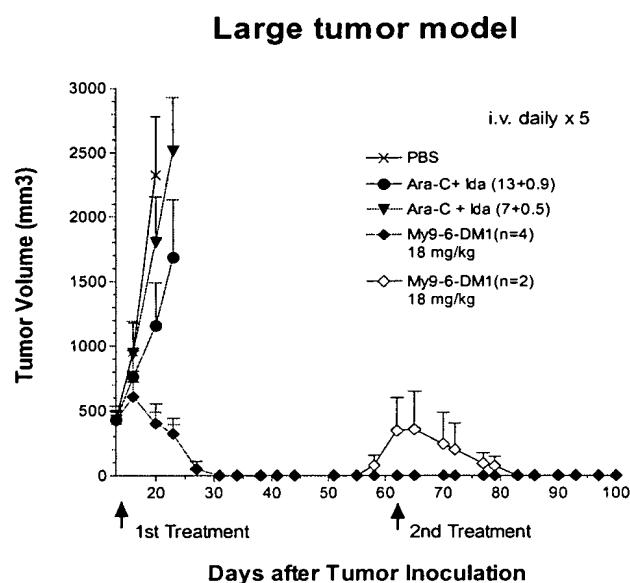


**B**



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**Figure 23A**



**Figure 23B**

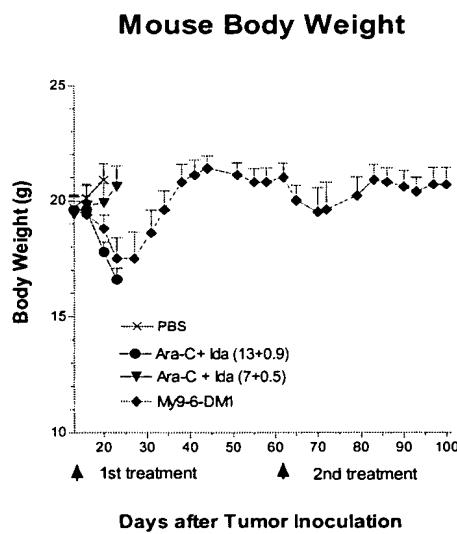


Figure 24A

**Efficacy of My9-6-DM1 in Survival model**

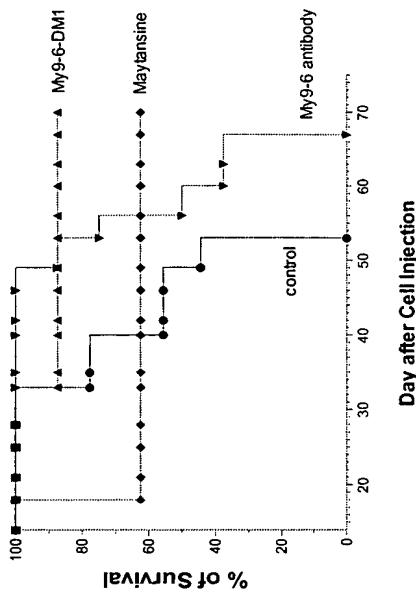


Figure 24B

**Comparison of My9-6-DM1 to Gemtuzumab Ozogamicin and standard chemotherapy**

